

Abstract

The invention concerns a method for the subtype-independent and/or species-independent detection of HI viruses in a sample using at least one oligonucleotide which contains at least 10 consecutive nucleotides from (i) a highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV, (ii) a corresponding region of another HI virus isolate, (iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto.